

JC17 Rec'd PCT/PTO 12 SEP 2005

AMENDED CLAIMS

1. (original) A nucleic acid which is replicatable in a microorganism of the family Corynebacterium and optionally a recombinant nucleic acid, characterized in that it has a nucleotide sequence coding for L-serine dehydratase which is partially or completely mutated or expressed to a lesser degree than the naturally occurring nucleotide sequence or which is not expressed at all.

2. (original) A nucleic acid according to claim 1, characterized in that the *sdaA* gene sequence is partially or completely deleted or mutated or expressed to a lesser extent by comparison with the naturally occurring sequence or not expressed at all.

3. (currently amended) A nucleic acid according to ~~one of claims 1 to 2~~ claim 1, characterized by a nucleotide sequence according to SEQ ID NO 1 whose nucleotides from position 506 to position 918 are completely or partially deleted or mutated, or an allele, homolog or derivative of this nucleotide sequence or a nucleotide sequence hybridizing therewith.

4. (currently amended) A nucleic acid according to ~~one of claims 1 to 3~~ claim 1, characterized in that it is isolated from a coryneform bacterium.

5. (currently amended) A nucleic acid according to ~~one of claims 1 to 4~~ claim 1, characterized in that it is isolated from *Corynebacterium* or *Brevibacterium*.

6. (currently amended) A nucleic acid according to ~~one of claims 1 to 5~~ claim 1, characterized in that it is isolated from *Corynebacterium glutamicum* or *Brevibacterium flavum*.

7. (currently amended) A gene structure containing at least one nucleotide sequence according to ~~claims 1 to 6~~ claim 1 and nucleotide sequences having regulatory sequences operatively linked therewith.

8. (currently amended) A vector containing at least one nucleotide sequence ~~according to claims 1 to 6~~ or a gene structure according to claim 7 and additional nucleotide sequences for selection, for replication in the host cell or for integration in the host cell genome.

9. (currently amended) L-serine dehydratase with reduced L-serine dehydratase activity coded with a nucleic acid according to ~~one of claims 1 to 6~~ claim 1.

10. (original) L-serine dehydratase according to claim 9 with an amino acid sequence according to sequence ID 2 whose

amino acid are altered in positions 135 to 274 or a modified form of this polypeptide sequence or an isoform thereof.

11. (currently amended) L-serine dehydratase according to ~~one of claims 9 to 10~~ claim 9, characterized in that it derives from coryneform bacteria.

12. (currently amended) L-serine dehydratase according to ~~one of claims 9 to 10~~ claim 9, characterized in that it derives from coryneform bacteria or brevibacteria.

13. (currently amended) L-serine dehydratase according to ~~one of claims 9 to 12~~ claim 9, characterized in that it derives from *Corynebacterium glutamicum* or *Brevibacterium flavum*.

14. (original) A microorganism characterized in that it has a nucleotide sequence which codes for an L-serine dehydratase, which is deleted in whole or in part or is mutated or is expressed to a reduced extent by comparison with the naturally occurring nucleotide sequence or is not expressed at all.

15. (original) A microorganism according to claim 14, characterized in that its *sdaA* gene is wholly or partially deleted or mutated or to a reduced extent by comparison with the naturally occurring *sdaA* gene or is not expressed at all.

16. (currently amended) A microorganism according to ~~one of claims 14 to 15~~ containing in replicatable form a nucleic acid according to ~~one of claims 1 to 6~~, a gene structure according to ~~claim 7~~, a vector according to ~~claim 8~~ or a polypeptide according to ~~claims 9 to 14~~ claim 1.

17. (currently amended) A microorganism according to ~~one of claims 14 to 16~~ claim 14, characterized in that it is a coryneform bacteria.

18. (currently amended) A microorganism according to ~~one of claims 14 to 17~~ claim 14, characterized in that it brings to the family a coryneform bacteria or brevibacteria.

19. (currently amended) A microorganism according to ~~one of claims 14 to 18~~ claim 14, characterized in that it brings to the family a *Corynebacterium glutamicum* or *Brevibacterium flavum*.

20. (currently amended) A probe for identifying and/or genes for coding which participate in the biosynthesis of L-serine characterized in that they are produced starting with nucleic acids according to ~~one of claims 1 to 6~~ claim 1 and contain a suitable marker for detection.

21. (original) A method for the microbial production of L-serine characterized in that

(a) a genetically altered microorganism is produced in which the nucleic acid in the microorganism coding for the L-serine dehydratase is partially or completely deleted or mutated or expressed to a reduced extent by comparison with the naturally occurring nucleic acid or is not expressed at all,

(b) this genetically altered microorganism from step (a) is used for microbial production, and

(c) the L-serine formed is isolated from the culture medium.

22. (original) The method according to claim 21, characterized in that the *sdaA* gene sequence is partially or completely deleted or mutated or expressed to a reduced extent by comparison with the naturally occurring nucleotide sequence or is not expressed at all.

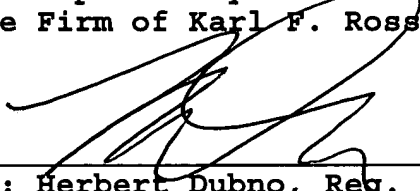
23. (currently amended) The method according to ~~one of~~ ~~claims 21 to 22~~ claim 21, characterized in that the nucleotide according to Sequence ID NO 1 is completely or partially deleted or mutated from position 506 to 918 or expressed to a reduced extent by comparison with the naturally occurring nucleotide sequence or not expressed at all.

24. (currently amended) The method according to ~~one of~~
~~claims 21 to 23~~ claim 21, characterized in that a microorganism
from the group of Corynebacterium, Brevibacterium, Arthrobacter,
Pseudomonas, Nocardia, Methylobacteria, Hyphomicrobium, Alkaligenes
or Klebsiella is used.

25. (currently amended) The A method wherein according
~~to one of claims 21 to 24, characterized in that~~ a nucleic acid
according to ~~claims 1 to 6 a gene structure according to claim 7 or~~
~~a vector according to claim 8~~ claim 1 is used.

This preliminary amendment is submitted to provide the cross reference of the present US phase of PCT/DE2004/000248 to the international application according to Rule 78 and to eliminate multiple dependencies in the claims.

Respectfully submitted,
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